cardiovascular_desease_prediction-GIT

December 3, 2023

[2]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from collections import Counter
import pickle

# Preprocess
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import LabelEncoder
from sklearn.impute import KNNImputer
from sklearn.model_selection import train_test_split

# Classification models
from sklearn.linear_model import LogisticRegression
from sklearn.naive_bayes import GaussianNB
from sklearn.neighbors import KNeighborsClassifier
from sklearn.neighbors import NearestCentroid
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from sklearn.ensemble import AdaBoostClassifier
from sklearn.ensemble import GradientBoostingClassifier
from sklearn.ensemble import HistGradientBoostingClassifier
from xgboost import XGBClassifier

# Metrics
from sklearn.metrics import accuracy_score
from sklearn.metrics import precision_score
from sklearn.metrics import recall_score
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay

# Hyperparametrization
from sklearn.model_selection import GridSearchCV
```

[3]:
```
df = pd.read_csv("cardio_train.csv", sep= ";")
```

[4]:
```
df_clean = df.copy()
```

1 1- EDA

[5]:
```
df_clean.head(3)
```

[5]:
```
   id    age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
0   0  18393       2     168    62.0    110     80            1     1      0
1   1  20228       1     156    85.0    140     90            3     1      0
2   2  18857       1     165    64.0    130     70            3     1      0

   alco  active  cardio
0     0       1       0
1     0       1       1
2     0       0       1
```

All of the dataset values were collected at the moment of medical examination.

Data description:

There are 3 types of input features: - 1- Objective Features (factual information): - age: Age of the pacient(days) | int - height: Height of the pacient(cm) | int - weight: Weight of the pacient(kg) | float - gender: Gender of the pacient | boolean

- 2- Examination Feature(results of medical examination):
  - ap_hi: Systolic blood pressure(mm Hg) | int
  - ap_lo: Diastolic blood pressure(mm Hg) | int
  - cholesterol: Cholesterol | categorical | 1: normal, 2: above normal, 3: well above normal
  - gluc: Glucose | categorical | 1: normal, 2: above normal, 3: well above normal
- 3- Subjective Feature(information given by the patient):
  - smoke: Smoking pacient | boolean
  - alco: Alcohol intake pacient | boolean
  - active: Physical activity | boolean

Target variable: - cardio: Presence or absence of cardiovascular disease | boolean

[6]:
```
df_clean.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 70000 entries, 0 to 69999
Data columns (total 13 columns):
 #   Column       Non-Null Count  Dtype
---  ------       --------------  -----
 0   id           70000 non-null  int64
 1   age          70000 non-null  int64
 2   gender       70000 non-null  int64
 3   height       70000 non-null  int64
 4   weight       70000 non-null  float64
 5   ap_hi        70000 non-null  int64
 6   ap_lo        70000 non-null  int64
 7   cholesterol  70000 non-null  int64
 8   gluc         70000 non-null  int64
 9   smoke        70000 non-null  int64
```

```
 10   alco         70000 non-null  int64
 11   active       70000 non-null  int64
 12   cardio       70000 non-null  int64
dtypes: float64(1), int64(12)
memory usage: 6.9 MB
```

[7]:
```python
df_clean.describe()
```

[7]:

	id	age	gender	height	weight
count	70000.000000	70000.000000	70000.000000	70000.000000	70000.000000
mean	49972.419900	19468.865814	1.349571	164.359229	74.205690
std	28851.302323	2467.251667	0.476838	8.210126	14.395757
min	0.000000	10798.000000	1.000000	55.000000	10.000000
25%	25006.750000	17664.000000	1.000000	159.000000	65.000000
50%	50001.500000	19703.000000	1.000000	165.000000	72.000000
75%	74889.250000	21327.000000	2.000000	170.000000	82.000000
max	99999.000000	23713.000000	2.000000	250.000000	200.000000

	ap_hi	ap_lo	cholesterol	gluc	smoke
count	70000.000000	70000.000000	70000.000000	70000.000000	70000.000000
mean	128.817286	96.630414	1.366871	1.226457	0.088129
std	154.011419	188.472530	0.680250	0.572270	0.283484
min	-150.000000	-70.000000	1.000000	1.000000	0.000000
25%	120.000000	80.000000	1.000000	1.000000	0.000000
50%	120.000000	80.000000	1.000000	1.000000	0.000000
75%	140.000000	90.000000	2.000000	1.000000	0.000000
max	16020.000000	11000.000000	3.000000	3.000000	1.000000

	alco	active	cardio
count	70000.000000	70000.000000	70000.000000
mean	0.053771	0.803729	0.499700
std	0.225568	0.397179	0.500003
min	0.000000	0.000000	0.000000
25%	0.000000	1.000000	0.000000
50%	0.000000	1.000000	0.000000
75%	0.000000	1.000000	1.000000
max	1.000000	1.000000	1.000000

!!¡¡ We can observe negative values in both systolic and diastolic blood pressure. Let's investigate these data:

- "ap_hi" Column:

[8]:
```python
df_clean[df_clean["ap_hi"]<0]
```

[8]:

	id	age	gender	height	weight	ap_hi	ap_lo	cholesterol	gluc
4607	6525	15281	1	165	78.0	-100	80	2	1
16021	22881	22108	2	161	90.0	-115	70	1	1

```
20536  29313  15581       1     153    54.0   -100     70             1      1
23988  34295  18301       1     162    74.0   -140     90             1      1
25240  36025  14711       2     168    50.0   -120     80             2      1
35040  50055  23325       2     168    59.0   -150     80             1      1
46627  66571  23646       2     160    59.0   -120     80             1      1

       smoke  alco  active  cardio
4607       0     0       1       0
16021      0     0       1       0
20536      0     0       1       0
23988      0     0       1       1
25240      0     0       0       1
35040      0     0       1       1
46627      0     0       0       0
```

[9]:
```python
df_clean[~df_clean["ap_hi"]<0]["ap_hi"].describe()
```

[9]:
```
count    69993.000000
mean       128.842241
std        153.998803
min          1.000000
25%        120.000000
50%        120.000000
75%        140.000000
max      16020.000000
Name: ap_hi, dtype: float64
```

We can see that there are 9 data points that most likely have been recorded with a negative sign by mistake, as they fall within a normal range. Let's change them to positive:

[10]:
```python
for idx in df_clean[df_clean["ap_hi"]<0].index:
    df_clean.loc[idx, "ap_hi"] *= -1
```

[11]:
```python
df_clean[df_clean["ap_hi"]<0]
```

[11]:
```
Empty DataFrame
Columns: [id, age, gender, height, weight, ap_hi, ap_lo, cholesterol, gluc,
smoke, alco, active, cardio]
Index: []
```

- "ap_lo" Column:

[12]:
```python
df_clean[df_clean["ap_lo"]<0]
```

[12]:
```
          id    age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  \
60106  85816  22571       1     167    74.0     15    -70            1     1
```

```
       smoke  alco  active  cardio
60106      0     0       1       1
```

[13]:
```
df_clean.loc[60106, "ap_lo"] *= -1
```

[14]:
```
df_clean[df_clean["ap_lo"]<0]
```

[14]:
```
Empty DataFrame
Columns: [id, age, gender, height, weight, ap_hi, ap_lo, cholesterol, gluc,
smoke, alco, active, cardio]
Index: []
```

1.1 1.1- Checking for duplicates:

[15]:
```
df_clean[df_clean.duplicated()]
```

[15]:
```
Empty DataFrame
Columns: [id, age, gender, height, weight, ap_hi, ap_lo, cholesterol, gluc,
smoke, alco, active, cardio]
Index: []
```

There's no duplicated rows

1.2 1.2- Outliers:

!!¡¡ We also observe potential outliers in the maximum values of some variables. Let's take a look:

[16]:
```
df_outliers = df_clean.copy()
```

[17]:
```
df_outliers.head(3)
```

[17]:
```
   id    age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
0   0  18393       2     168    62.0    110     80            1     1      0
1   1  20228       1     156    85.0    140     90            3     1      0
2   2  18857       1     165    64.0    130     70            3     1      0

   alco  active  cardio
0     0       1       0
1     0       1       1
2     0       0       1
```

[18]:
```
# Let's transform "age" column to years:
df_outliers["age"] = df_outliers["age"].apply(lambda x: x/365)
```

[19]:
```
df_outliers[["age", "height", "weight", "ap_hi", "ap_lo"]].describe()
```

[19]:
```
                age        height        weight         ap_hi         ap_lo
count  70000.000000  70000.000000  70000.000000  70000.000000  70000.000000
```

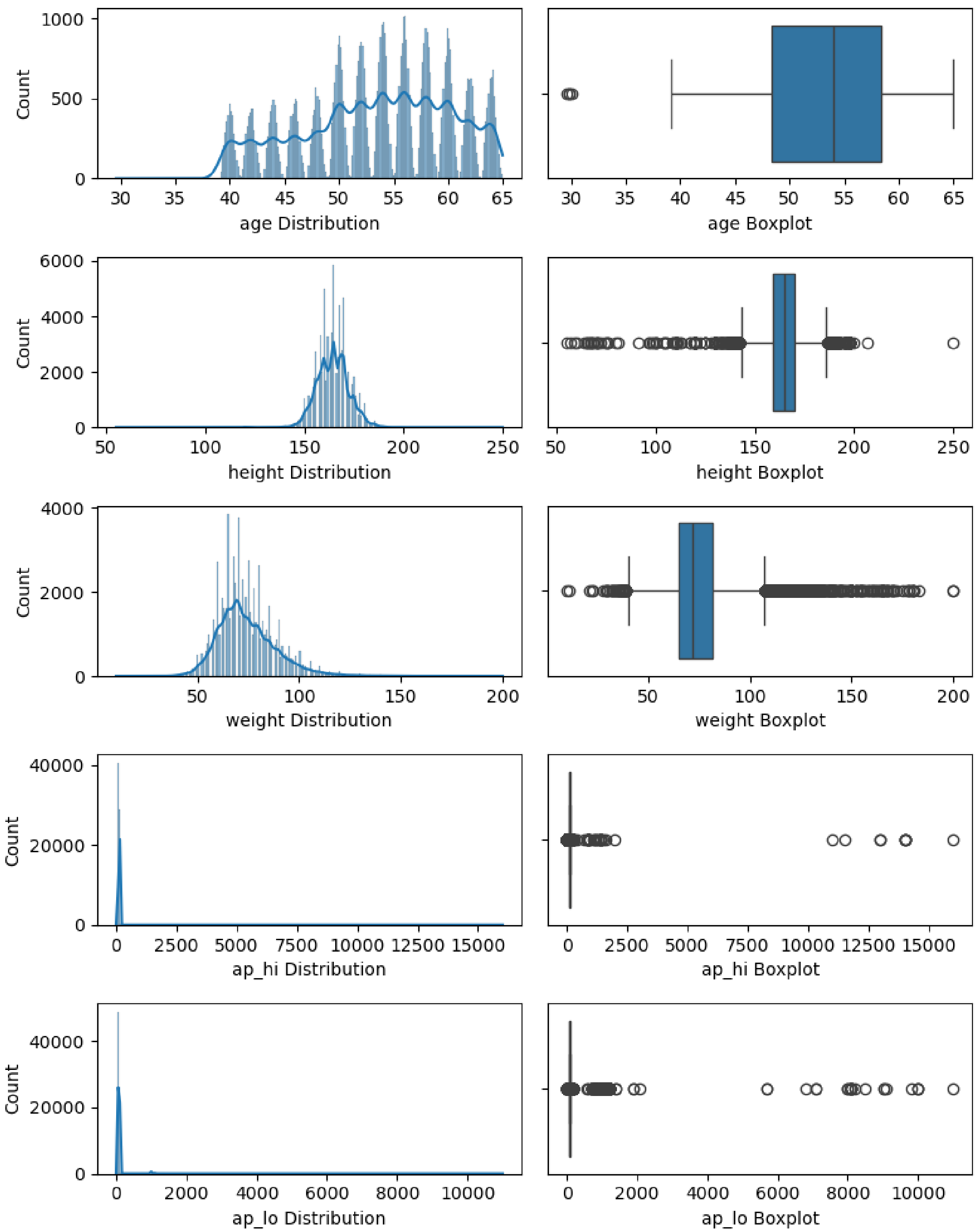
mean	53.339358	164.359229	74.205690	128.841429	96.632414
std	6.759594	8.210126	14.395757	153.991223	188.471505
min	29.583562	55.000000	10.000000	1.000000	0.000000
25%	48.394521	159.000000	65.000000	120.000000	80.000000
50%	53.980822	165.000000	72.000000	120.000000	80.000000
75%	58.430137	170.000000	82.000000	140.000000	90.000000
max	64.967123	250.000000	200.000000	16020.000000	11000.000000

[20]:
```
fig, ax =  plt.subplots(5, 2, figsize = (8, 10))
ax = ax.flatten()

num_graph = [i for i in range(ax.size) if i%2 == 0]
columns = ["age", "height", "weight", "ap_hi", "ap_lo"]
num_bins = int(np.sqrt(len(df_outliers)))

for idx, column in zip(num_graph, columns):
    sns.histplot(x = df_outliers[column], bins = num_bins, kde = True, ax =␣
 ↪ax[idx])
    ax[idx].set_xlabel(column + ' Distribution')
    sns.boxplot(x = df_outliers[column], ax = ax[idx+1])
    ax[idx+1].set_xlabel(column + ' Boxplot')

plt.tight_layout()
plt.show()
```



!¡!¡ Let's first address the outliers in the 'ap_hi' and 'ap_lo' columns, as they are the most significant. To do this, we will consider the following: The European Society of Cardiology divides blood pressure levels into three categories:

- Optimal: Systolic pressure less than 120 mmHg and diastolic pressure less than 80 mmHg.

- Normal: Systolic pressure between 120-129 mmHg and/or diastolic pressure between 80-84 mmHg.
- High-normal: Systolic pressure between 130/85 mmHg and/or diastolic pressure between 139/89 mmHg.

Based on these values, three grades of hypertension are defined:

- Grade 1 Hypertension: **Systolic pressure** 140-159 mmHg and/or **diastolic pressure** 90-99 mmHg.
- Grade 2 Hypertension: **Systolic pressure** 160-179 mmHg and/or **diastolic pressure** 100-109 mmHg.
- Grade 3 Hypertension: **Systolic pressure** greater than or equal to 180 mmHg and/or **diastolic pressure** greater than or equal to 110 mmHg.

[21]:
```
def outliers(variable):
    '''
    Function to obtain the upper and lower limits after calculating the␣
 ↪interquartile range.
    '''
    Q1 = variable.quantile(q = 0.25)
    Q3 = variable.quantile(q = 0.75)

    # Rango intercuartil (IQR)
    IQR = Q3 - Q1

    # Calcular los limites inferior y superior
    lim_inf = Q1 - 1.5 * IQR
    lim_sup = Q3 + 1.5 * IQR

    return lim_inf, lim_sup
```

1.2.1- "ap_hi" Column (_1):

[22]:
```
lim_inf_1, lim_sup_1 = outliers(df_outliers["ap_hi"])
print(f"Lower limit: {lim_inf_1}\nUpper limit: {lim_sup_1}")
```

```
Lower limit: 90.0
Upper limit: 170.0
```

Guided by the previously provided information, we define the maximum and minimum limits for systolic blood pressure as 210 and 90 mmHg, respectively:

[23]:
```
percentage_outliers_ap_hi = len(df_outliers[(~df_outliers["ap_hi"].
 ↪between(lim_inf_1, 210))])*100/len(df_outliers)
print(f"Percentage of outliers in the 'ap_hi' column:␣
 ↪{round(percentage_outliers_ap_hi, 2)} %")
```

```
Percentage of outliers in the 'ap_hi' column: 0.55 %
```

Approaches: - A. Removal of outliers (0.56%) - B. We can define outliers as NaN's, so after cleaning the dataframe, we can impute them using KNNImputer.

!¡!¡ In an attempt to avoid losing information in a relevant column, option B is chosen.

1.2.2- “ap_lo” Column (_2):

```
[24]: lim_inf_2, lim_sup_2 = outliers(df_outliers["ap_lo"])
      print(f"Lower limit: {lim_inf_2}\nUpper limit: {lim_sup_2}")
```

```
Lower limit: 65.0
Upper limit: 105.0
```

In this case, we define the maximum and minimum limits for diastolic blood pressure as 140 and 50 mmHg, respectively:

```
[25]: percentage_outliers_ap_lo = len(df_outliers[(~df_outliers["ap_lo"].between(50,␣
       ↪140))])*100/len(df_outliers)
      print(f"Percentage of outliers in the 'ap_lo' column:␣
       ↪{round(percentage_outliers_ap_lo,2)} %")
```

```
Percentage of outliers in the 'ap_lo' column: 1.52 %
```

Note that values start to spike after 190, likely due to annotation errors. Approaches: - A. Removal of outliers (1.52%) - B. We can define outliers as NaN’s, so after cleaning the dataframe, we can impute them using KNNImputer.

!¡!¡ In an attempt to avoid losing information in a relevant column, option B is chosen.

1.2.3- “height” Column (_3):

```
[26]: lim_inf_3, lim_sup_3 = outliers(df_outliers["height"])
      print(f"Lower limit: {lim_inf_3}\nUpper limit: {lim_sup_3}")
```

```
Lower limit: 142.5
Upper limit: 186.5
```

```
[27]: percentage_outliers_height = len(df_outliers[(~df_outliers["height"].
       ↪between(lim_inf_3, 200))])*100/len(df_outliers)
      print(f"Percentage of outliers in the 'height' column:␣
       ↪{round(percentage_outliers_height,2)} %")
```

```
Percentage of outliers in the 'height' column: 0.36 %
```

```
[28]: df_outliers[df_outliers["height"] > 200].sort_values(by= "height",␣
       ↪ascending=True)
```

[28]:

```
          id        age  gender  height  weight  ap_hi  ap_lo  cholesterol  \
21628  30894  52.202740       2     207    78.0    100     70            1
6486    9223  58.136986       1     250    86.0    140    100            3

       gluc  smoke  alco  active  cardio
21628     1      0     1       1       0
6486      1      0     0       1       1
```

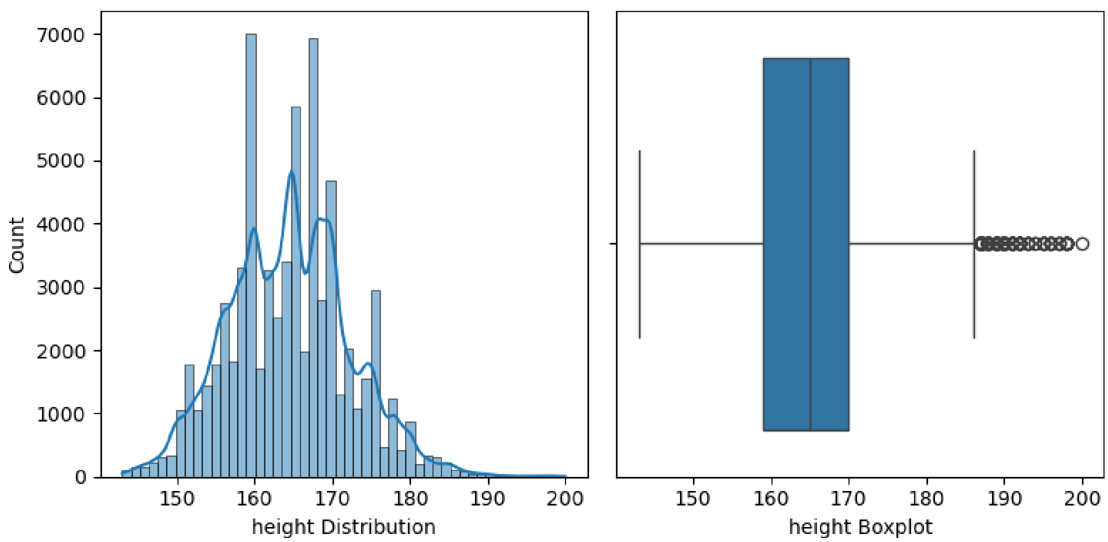
[29]:
```
# Removing outliers:
column_3 = "height"

df_outliers = df_outliers[df_outliers[column_3].between(lim_inf_3, 200)]

# Plot:
fig, ax =  plt.subplots(1, 2, figsize = (8, 4))
ax = ax.flatten()

sns.histplot(x = df_outliers[column_3], bins = 50, kde = True, ax = ax[0])
ax[0].set_xlabel(column_3 + ' Distribution')
sns.boxplot(x = df_outliers[column_3], ax = ax[1])
ax[1].set_xlabel(column_3 + ' Boxplot')

plt.tight_layout()
plt.show()
```



1.2.4- "weight" Column (_4): *!¡!¡ It's important to note that overweight is a risk factor for cardiovascular diseases. Therefore, high weights that are not considered anomalies (errors) will not be removed. However, weights below the lower limit will be removed.*

[30]:
```
lim_inf_4, lim_sup_4 = outliers(df_outliers["weight"])
print(f"Lower limit: {lim_inf_4}\nUpper limit: {lim_sup_4}")
```

```
Lower limit: 39.5
Upper limit: 107.5
```

[31]:
```
percentage_outliers_weight = len(df_outliers[(df_outliers["weight"] <␣
  ↪lim_inf_4)])*100/len(df_outliers)
```

```python
print(f"Percentage of outliers below 39.5 Kg in the 'weight' column:␣
↪{round(percentage_outliers_weight,2)} %")
```

```
Percentage of outliers below 39.5 Kg in the 'weight' column: 0.06 %
```

[32]:
```python
df_outliers["weight"].describe()
```

[32]:
```
count    69748.000000
mean        74.217507
std         14.341027
min         10.000000
25%         65.000000
50%         72.000000
75%         82.000000
max        200.000000
Name: weight, dtype: float64
```

[402]:
```python
df_outliers[df_outliers["weight"] > 82]["cardio"].value_counts()
```

[402]:
```
cardio
1    10586
0     6204
Name: count, dtype: int64
```

It's observed that patients weighing more than 82 kg have a 62% higher likelihood of experiencing cardiovascular problems.

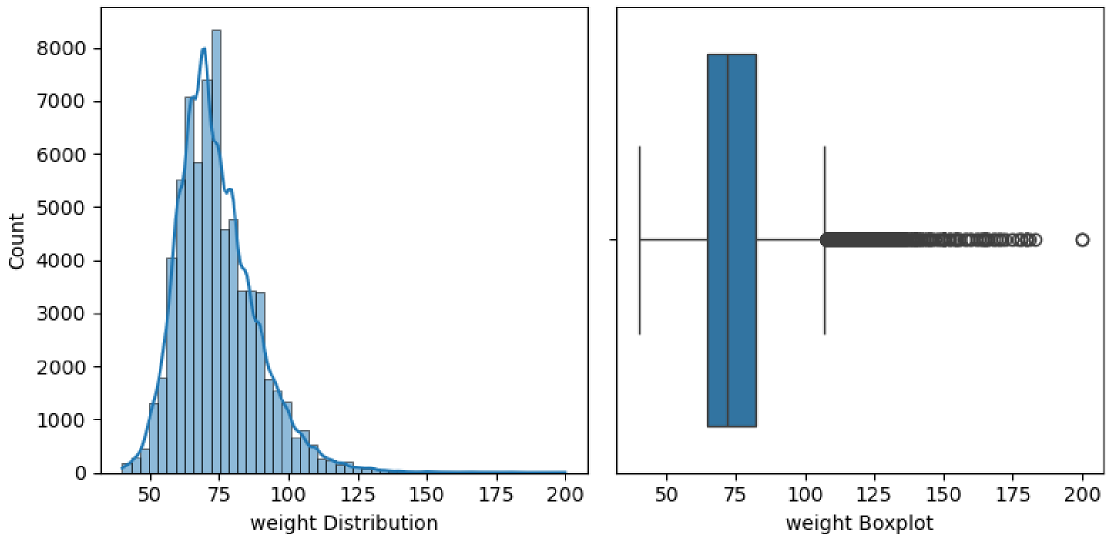
[403]:
```python
# Removing outliers:
column_4 = "weight"

df_outliers = df_outliers[df_outliers[column_4] > lim_inf_4]

# Grafico:
fig, ax =  plt.subplots(1, 2, figsize = (8, 4))
ax = ax.flatten()

sns.histplot(x = df_outliers[column_4], bins = 50, kde = True, ax = ax[0])
ax[0].set_xlabel(column_4 + ' Distribution')
sns.boxplot(x = df_outliers[column_4], ax = ax[1])
ax[1].set_xlabel(column_4 + ' Boxplot')

plt.tight_layout()
plt.show()
```



1.3 1.3- Checking for class imbalance:

[33]:
```
clases = df_outliers["cardio"].value_counts()
clases_dict = clases.to_dict()
```

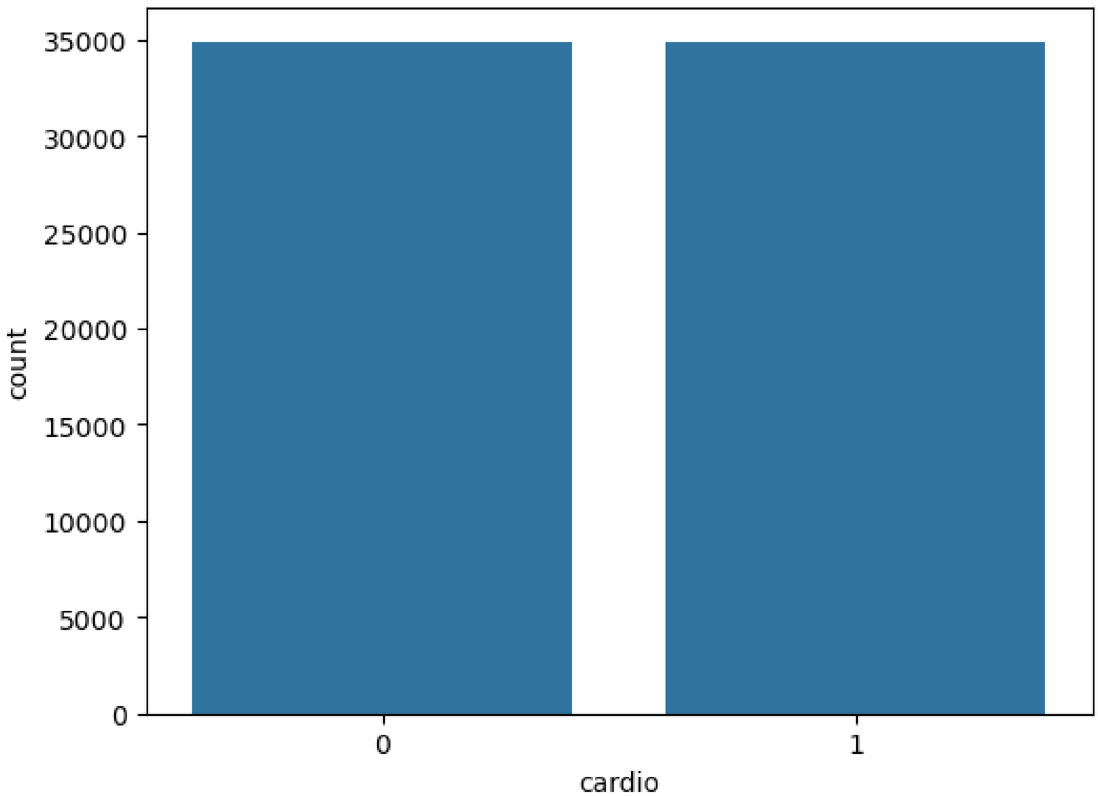
[34]:
```
no_cardio = clases_dict[0]*100/clases.values.sum()
cardio = clases_dict[1]*100/clases.values.sum()

print(f"Percentage of patients without cardiovascular problems:␣
↪{round(no_cardio, 2)} % \nPercentage of patients with cardiovascular␣
↪problems: {round(cardio, 2)} %")
```

```
Percentage of patients without cardiovascular problems: 50.04 %
Percentage of patients with cardiovascular problems: 49.96 %
```

There is no class imbalance.

[35]:
```
sns.barplot(clases);
```



1.4 1.4 Let's analyze the subjective columns:

[407]:
```
df_outliers[["smoke", "alco", "active"]].head(3)
```

[407]:

	smoke	alco	active
0	0	0	1
1	0	0	1
2	0	0	0

Let's see if there are differences between people with healthy habits and those who have some type of unhealthy habit in relation to cardiovascular problems. If noticeable differences exist, we will keep these columns for further analysis.

- We define a healthy person as someone who does not smoke (0), does not drink (0), and is active (1).
- We define an unhealthy person as someone who has any unhealthy habit.

- Percentage of people with healthy habits:

[408]:
```
healthy_mask = (df_outliers["smoke"] == 0) & (df_outliers["alco"] == 0) &␣
↪(df_outliers["active"] == 1)
percentage_healthy = len(df_outliers[healthy_mask]) * 100 / len(df_outliers)
```

```
print(f"Percentage of healthy: {round(percentage_healthy)}%")
```

```
Percentage of healthy: 71%
```

[409]:
```
total_cardio_healthy = df_outliers[healthy_mask]["cardio"].value_counts()
percentage_cardio_healthy = total_cardio_healthy[1]*100/total_cardio_healthy.
  ↪sum()
print(f"Percentage of deseasse if healthy: {round(percentage_cardio_healthy)}%")
```

```
Percentage of deseasse if healthy: 49%
```

- Percentage of people with unhealthy habits:

[410]:
```
no_healthy_mask = (df_outliers["smoke"] == 1) | (df_outliers["alco"] == 1) |␣
  ↪(df_outliers["active"] == 0)
percentage_no_healthy = len(df_outliers[no_healthy_mask]) * 100 /␣
  ↪len(df_outliers)
print(f"Percentage of no healthy: {round(percentage_no_healthy)}%")
```

```
Percentage of no healthy: 29%
```

[411]:
```
total_cardio_no_healthy = df_outliers[no_healthy_mask]["cardio"].value_counts()
percentage_cardio_no_healthy = total_cardio_no_healthy[1]*100/
  ↪total_cardio_no_healthy.sum()
print(f"Percentage of deseasse if no healthy:␣
  ↪{round(percentage_cardio_no_healthy)}%")
```

```
Percentage of deseasse if no healthy: 52%
```

- *We can observe that people with healthy habits have a lower percentage of cardiovascular problems, although the difference is not significant compared to those with some type of unhealthy habit.*

As there is a small difference between habits, we will consider the subjective columns for this analysis, as they may contribute predictive information.

2 2- Data Preprocessing

[412]:
```
df_preprocess = df_outliers.copy()
```

[413]:
```
df_preprocess.head(3)
```

[413]:
```
   id        age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  \
0   0  50.391781       2     168    62.0    110     80            1     1
1   1  55.419178       1     156    85.0    140     90            3     1
2   2  51.663014       1     165    64.0    130     70            3     1

   smoke  alco  active  cardio
0      0     0       1       0
1      0     0       1       1
```

```
2      0     0       0       1
```

[414]:
```
df_preprocess.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 69703 entries, 0 to 69999
Data columns (total 13 columns):
 #   Column       Non-Null Count  Dtype
---  ------       --------------  -----
 0   id           69703 non-null  int64
 1   age          69703 non-null  float64
 2   gender       69703 non-null  int64
 3   height       69703 non-null  int64
 4   weight       69703 non-null  float64
 5   ap_hi        69703 non-null  int64
 6   ap_lo        69703 non-null  int64
 7   cholesterol  69703 non-null  int64
 8   gluc         69703 non-null  int64
 9   smoke        69703 non-null  int64
 10  alco         69703 non-null  int64
 11  active       69703 non-null  int64
 12  cardio       69703 non-null  int64
dtypes: float64(2), int64(11)
memory usage: 7.4 MB
```

2.1 2.1- OneHot encoding:

[415]:
```
gender_dic = {x : num for num, x in enumerate(df_preprocess["gender"].unique())}

df_preprocess["gender"] = df_preprocess["gender"].map(gender_dic)
```

2.2 2.2- Label encoding:

- "cholesterol" Column:

[416]:
```
cholesterol_label_encoder = LabelEncoder()

cholesterol = cholesterol_label_encoder.
 ↪fit_transform(df_preprocess["cholesterol"])

df_preprocess["cholesterol"] = cholesterol
```

- "gluc" Column:

[417]:
```
gluc_label_encoder = LabelEncoder()

gluc = gluc_label_encoder.fit_transform(df_clean["gluc"])
```

```
df_clean["gluc"] = gluc
```

[418]:
```
df_preprocess.head(3)
```

[418]:
```
   id        age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  \
0   0  50.391781       0     168    62.0    110     80            0     1
1   1  55.419178       1     156    85.0    140     90            2     1
2   2  51.663014       1     165    64.0    130     70            2     1

   smoke  alco  active  cardio
0      0     0       1       0
1      0     0       1       1
2      0     0       0       1
```

2.3 2.3- Converting the values in the 'height' column to the International System of Units:

- Height to meters

[419]:
```
def to_meter(x):
    x_meter = x/100
    return x_meter
```

[420]:
```
df_preprocess["height"] = df_preprocess["height"].apply(to_meter)
```

[421]:
```
df_preprocess.head(3)
```

[421]:
```
   id        age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  \
0   0  50.391781       0    1.68    62.0    110     80            0     1
1   1  55.419178       1    1.56    85.0    140     90            2     1
2   2  51.663014       1    1.65    64.0    130     70            2     1

   smoke  alco  active  cardio
0      0     0       1       0
1      0     0       1       1
2      0     0       0       1
```

2.4 2.4- Creation of new variables:

- Body Mass Index:

[422]:
```
df_preprocess["IMC"] = df_preprocess["weight"] / (df_preprocess["height"])**2
```

[423]:
```
df_preprocess.head(3)
```

[423]:
```
   id        age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  \
0   0  50.391781       0    1.68    62.0    110     80            0     1
1   1  55.419178       1    1.56    85.0    140     90            2     1
```

```
2   2  51.663014       1     1.65     64.0     130      70              2      1

   smoke  alco  active  cardio         IMC
0      0     0       1       0  21.967120
1      0     0       1       1  34.927679
2      0     0       0       1  23.507805
```

2.5 2.5- Data type transformation:

[424]:
```python
df_preprocess.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 69703 entries, 0 to 69999
Data columns (total 14 columns):
 #   Column       Non-Null Count  Dtype
---  ------       --------------  -----
 0   id           69703 non-null  int64
 1   age          69703 non-null  float64
 2   gender       69703 non-null  int64
 3   height       69703 non-null  float64
 4   weight       69703 non-null  float64
 5   ap_hi        69703 non-null  int64
 6   ap_lo        69703 non-null  int64
 7   cholesterol  69703 non-null  int64
 8   gluc         69703 non-null  int64
 9   smoke        69703 non-null  int64
 10  alco         69703 non-null  int64
 11  active       69703 non-null  int64
 12  cardio       69703 non-null  int64
 13  IMC          69703 non-null  float64
dtypes: float64(4), int64(10)
memory usage: 8.0 MB
```

[425]:
```python
cols_to_int = ["gender", "ap_hi", "ap_lo", "cholesterol", "gluc", "smoke",␣
↪"alco", "active", "cardio"]

for col in cols_to_int:
    df_preprocess[col] = df_preprocess[col].astype("int")
```

[426]:
```python
df_preprocess.info()
```

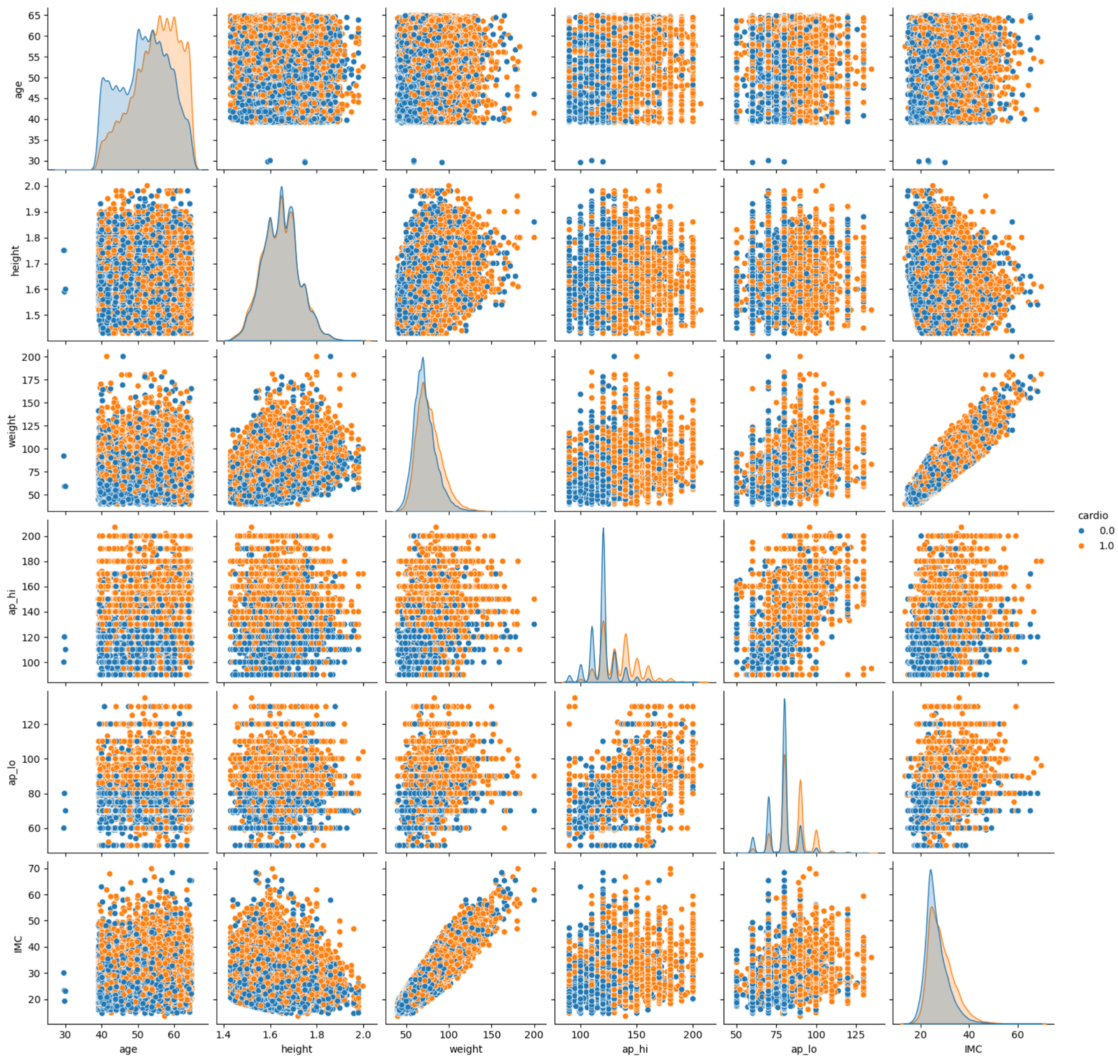
```
<class 'pandas.core.frame.DataFrame'>
Index: 69703 entries, 0 to 69999
Data columns (total 14 columns):
 #   Column       Non-Null Count  Dtype
---  ------       --------------  -----
 0   id           69703 non-null  int64
 1   age          69703 non-null  float64
```

```
 2   gender       69703 non-null  int32
 3   height       69703 non-null  float64
 4   weight       69703 non-null  float64
 5   ap_hi        69703 non-null  int32
 6   ap_lo        69703 non-null  int32
 7   cholesterol  69703 non-null  int32
 8   gluc         69703 non-null  int32
 9   smoke        69703 non-null  int32
 10  alco         69703 non-null  int32
 11  active       69703 non-null  int32
 12  cardio       69703 non-null  int32
 13  IMC          69703 non-null  float64
dtypes: float64(4), int32(9), int64(1)
memory usage: 5.6 MB
```

2.6 2.6 Correlation analysis:

[369]:
```
sns.pairplot(data = df_preprocess, vars=["age", "height", "weight", "ap_hi",␣
↪"ap_lo", "IMC"], hue = "cardio");
```

```
C:\Users\regue\conda_ENV\Lib\site-packages\seaborn\axisgrid.py:123: UserWarning:
The figure layout has changed to tight
  self._figure.tight_layout(*args, **kwargs)
```



"The height column DOES NOT seem to show a correlation with cardiovascular problems, so we will remove it.

2.7 2.7- Column deletion:

[427]:
```
df_preprocess = df_preprocess.drop(["id", "height"], axis= 1)
```

[428]:
```
df_preprocess.head(3)
```

[428]:
```
         age  gender  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  alco  \
0  50.391781       0    62.0    110     80            0     1      0     0
1  55.419178       1    85.0    140     90            2     1      0     0
2  51.663014       1    64.0    130     70            2     1      0     0

   active  cardio        IMC
```

```
0         1         0   21.967120
1         1         1   34.927679
2         0         1   23.507805
```

2.8 2.8- Imputing values for the 'ap_hi' and 'ap_lo' columns (Option B - Section 1.2.1 and 1.2.2):

I'll convert the values of systolic and diastolic blood pressure to NaN and then impute them using the KNNImputer. - For systolic blood pressure ('ap_hi'), values outside the range of 90 to 210 mmHg will be converted to NaN. - For diastolic blood pressure ('ap_lo'), values outside the range of 50 to 140 mmHg will be converted to NaN.

[429]:
```
limite_sup_SI_ap_hi = 210
limite_inf_SI_ap_hi = 90

percentage_outliers_ap_hi = len(df_preprocess[(~df_preprocess["ap_hi"].
 ↪between(limite_inf_SI_ap_hi, limite_sup_SI_ap_hi))])*100/len(df_preprocess)
print(f"Percentage of outliers in the 'ap_hi' column:␣
 ↪{round(percentage_outliers_ap_hi,2)} %")
```

```
Percentage of outliers in the 'ap_hi' column: 0.55 %
```

[430]:
```
limite_sup_SI_ap_lo = 140
limite_inf_SI_ap_lo = 50

percentage_outliers_ap_lo = len(df_preprocess[(~df_preprocess["ap_lo"].
 ↪between(limite_inf_SI_ap_lo, limite_sup_SI_ap_lo))])*100/len(df_preprocess)
print(f"Percentage of outliers in the 'ap_lo' column:␣
 ↪{round(percentage_outliers_ap_lo,2)} %")
```

```
Percentage of outliers in the 'ap_lo' column: 1.51 %
```

[431]:
```
# Defining NaN:
df_preprocess["ap_hi"] = df_preprocess["ap_hi"].apply(lambda x: np.nan if not␣
 ↪(limite_inf_SI_ap_hi <= x < limite_sup_SI_ap_hi) else x)
df_preprocess["ap_lo"] = df_preprocess["ap_lo"].apply(lambda x: np.nan if not␣
 ↪(limite_inf_SI_ap_lo <= x < limite_sup_SI_ap_lo) else x)
```

[432]:
```
df_preprocess[["ap_hi", "ap_lo"]].isna().sum()
```

[432]:
```
ap_hi     409
ap_lo    1087
dtype: int64
```

[433]:
```
presion_imputer = KNNImputer()
df_preprocess = pd.DataFrame(data = presion_imputer.
 ↪fit_transform(df_preprocess), columns = df_preprocess.columns)
df_preprocess.head(3)
```

[433]:
```
         age  gender  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  alco  \
0  50.391781     0.0    62.0  110.0   80.0          0.0   1.0    0.0   0.0
1  55.419178     1.0    85.0  140.0   90.0          2.0   1.0    0.0   0.0
2  51.663014     1.0    64.0  130.0   70.0          2.0   1.0    0.0   0.0

   active  cardio        IMC
0     1.0     0.0  21.967120
1     1.0     1.0  34.927679
2     0.0     1.0  23.507805
```

[434]:
```
df_preprocess[["ap_hi", "ap_lo"]].isna().sum()
```

[434]:
```
ap_hi    0
ap_lo    0
dtype: int64
```

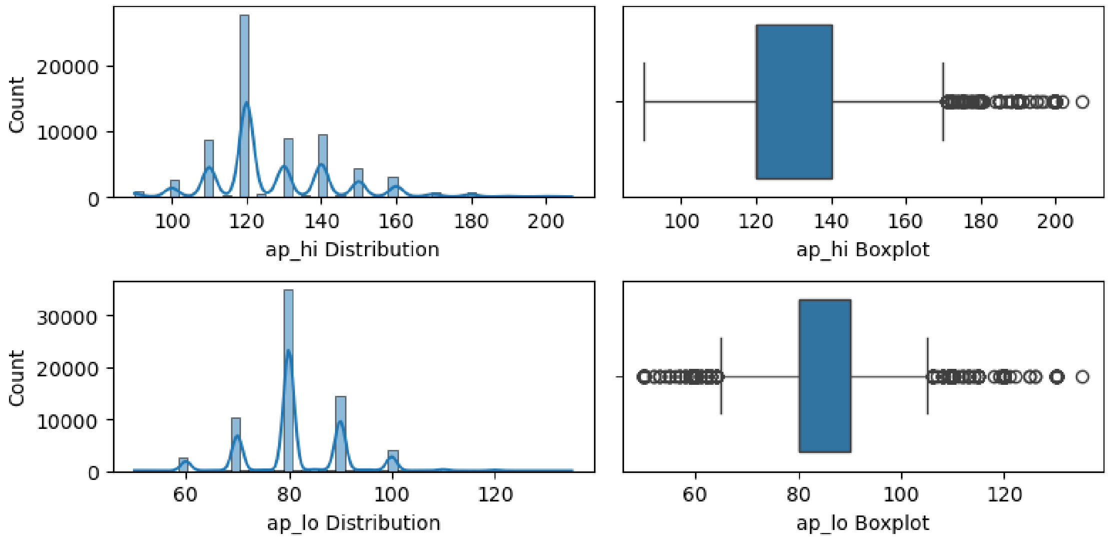
[435]:
```
# Plot:
column_1= "ap_hi"
column_2= "ap_lo"

fig, ax =  plt.subplots(2, 2, figsize = (8, 4))
ax = ax.flatten()

# Systolic blood pressure:
sns.histplot(x = df_preprocess[column_1], bins = 50, kde = True, ax = ax[0])
ax[0].set_xlabel(column_1 + ' Distribution')
sns.boxplot(x = df_preprocess[column_1], ax = ax[1])
ax[1].set_xlabel(column_1 + ' Boxplot')

# Diastolic blood pressure:
sns.histplot(x = df_preprocess[column_2], bins = 50, kde = True, ax = ax[2])
ax[2].set_xlabel(column_2 + ' Distribution')
sns.boxplot(x = df_preprocess[column_2], ax = ax[3])
ax[3].set_xlabel(column_2 + ' Boxplot')

plt.tight_layout()
plt.show()
```



2.9 2.8- Feature Selection

[436]:
```python
df_processed = df_preprocess.copy()
```

[437]:
```python
# df_processed.to_csv("cardio_data_processed_final.csv", index= False, sep= ",")
```

[438]:
```python
df_processed = pd.read_csv("cardio_data_processed_final.csv")
```

[439]:
```python
df_processed.head(3)
```

[439]:
```
         age  gender  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  alco  \
0  50.391781     0.0    62.0  110.0   80.0          0.0   1.0    0.0   0.0
1  55.419178     1.0    85.0  140.0   90.0          2.0   1.0    0.0   0.0
2  51.663014     1.0    64.0  130.0   70.0          2.0   1.0    0.0   0.0

   active  cardio        IMC
0     1.0     0.0  21.967120
1     1.0     1.0  34.927679
2     0.0     1.0  23.507805
```

[440]:
```python
df_processed = df_processed.sample(frac=1, random_state=42)

X = df_processed.drop(["cardio"], axis = 1)
y = df_processed["cardio"]

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.2,␣
↪stratify= y, random_state = 42)

# Scale:
```

```
scaler_x = StandardScaler()

X_train_scaled = scaler_x.fit_transform(X_train)
X_test_scaled = scaler_x.transform(X_test)
```

3 3- Training models:

[441]:
```
models = [LogisticRegression(), GaussianNB(), KNeighborsClassifier(),␣
 ↪NearestCentroid(), RandomForestClassifier(), SVC(), AdaBoostClassifier(),␣
 ↪GradientBoostingClassifier(), XGBClassifier(),␣
 ↪HistGradientBoostingClassifier()]
```

[ ]:
```
%%time

resultados = []

for model in models:

    model.fit(X_train_scaled, y_train)
    y_pred = model.predict(X_test_scaled)

    # Metricas:
    accuracy = accuracy_score(y_test, y_pred)
    precision = precision_score(y_test, y_pred)
    recall = recall_score(y_test, y_pred)

    resultados.append([str(model), accuracy, precision, recall])

df_resultados = pd.DataFrame(resultados, columns= ["Modelo", "Accuracy",␣
 ↪"Precision", "Recall"])
```

[443]:
```
df_resultados.sort_values(by="Accuracy", ascending=False)
```

[443]:
```
                                              Modelo  Accuracy  Precision  \
7                       GradientBoostingClassifier()  0.743993   0.764276
9                   HistGradientBoostingClassifier()  0.743275   0.759222
5                                              SVC()  0.742630   0.773124
6                               AdaBoostClassifier()  0.740119   0.780972
8  XGBClassifier(base_score=None, booster=None, c…  0.739258   0.759788
0                               LogisticRegression()  0.736102   0.764867
3                                  NearestCentroid()  0.722186   0.747559
4                           RandomForestClassifier()  0.719963   0.725346
1                                       GaussianNB()  0.710925   0.757544
2                             KNeighborsClassifier()  0.700739   0.702288

     Recall
```

```
7   0.705139
9   0.712030
5   0.686334
6   0.666954
8   0.699254
0   0.681309
3   0.670399
4   0.707436
1   0.619868
2   0.696239
```

3.1 3.1- Hyperparametrization:

3.1.1 3.1.1- Gradient Boosting Classifier

[576]:
```
model_GBC = GradientBoostingClassifier()

parameters_GBC = {"learning_rate"           : [0.09], # Probar > 0.08
                  "loss"                    : ['log_loss'],
                  "n_estimators"            : [250],
                  "subsample"               : [1],
                  "min_impurity_decrease"   : [0.05],
                  "max_depth"               : [3]}
                  #"max_features"            : [None],
                  #"min_samples_leaf"        : [1],
                  #"min_samples_split"       : [3]}
```

[ ]:
```
%%time

resultados_GBC = []

grid_solver_GBC = GridSearchCV(estimator      = model_GBC,
                               param_grid     = parameters_GBC,
                               scoring        = "accuracy",
                               refit          = "accuracy",
                               cv             = 5,
                               n_jobs         = -1,
                               verbose        = 2)

model_result_GBC = grid_solver_GBC.fit(X_train_scaled, y_train)


y_pred = model_result_GBC.best_estimator_.predict(X_test_scaled)

params_GBC = model_result_GBC.best_estimator_.get_params()

# Metrics:
```

```
accuracy = accuracy_score(y_test, y_pred)
precision = precision_score(y_test, y_pred)
recall = recall_score(y_test, y_pred)

resultados_GBC.append([str(model_GBC), accuracy, precision, recall, params_GBC])
resultados.append([str(model_GBC), accuracy, precision, recall, params_GBC])

df_resultados_GBC = pd.DataFrame(resultados_GBC, columns= ["Modelo",␣
↪"Accuracy", "Precision", "Recall", "Parameters"])
```

[ ]:
```
##########################################################################################
```

3.1.2 3.1.2- Random Forest Classifier

[89]:
```
model_RFC = RandomForestClassifier()

parameters_RFC = {"n_estimators"           : [50, 100, 200],
                  "criterion"              : ["gini", "entropy"],
                  "max_depth"              : [3, 4, 5],
                  "max_features"           : [2, 3],
                  "max_leaf_nodes"         : [None, 8],
                  "min_impurity_decrease"  : [0, 0.02, 0.3],
                  "min_samples_split"      : [2, 3, 5]}
```

[ ]:
```
%%time

resultados_RFC = []

grid_solver_RFC = GridSearchCV(estimator      = model_RFC,
                               param_grid     = parameters_RFC,
                               scoring        = "accuracy",
                               cv             = 5,
                               verbose        = 2,
                               refit          = "accuracy",
                               n_jobs         = None)

model_result_RFC = grid_solver_RFC.fit(X_train_scaled, y_train)


y_pred = model_result_RFC.best_estimator_.predict(X_test_scaled)

params_RFC = model_result_RFC.best_estimator_.get_params()

# Metrics:
accuracy = accuracy_score(y_test, y_pred)
precision = precision_score(y_test, y_pred)
recall = recall_score(y_test, y_pred)
```

```python
resultados_RFC.append([str(model_RFC), accuracy, precision, recall, params_RFC])
resultados.append([str(model_RFC), accuracy, precision, recall, params_RFC])

df_resultados_RFC = pd.DataFrame(resultados_RFC, columns= ["Modelo",␣
 ↪"Accuracy", "Precision", "Recall", "Parameters"])
```

[ ]:
```python
##########################################################################################
```

3.1.3 3.1.3- Hist Gradient Boosting Classifier

[525]:
```python
model_HGBC = HistGradientBoostingClassifier()

parameters_HGBC = {"learning_rate"       : [0.05],
                   "max_iter"            : [100,200,10],
                   "max_leaf_nodes"      : [24],
                   "max_depth"           : [None],
                   "min_samples_leaf"    : [16]}
```

[ ]:
```python
%%time

resultados_HGBC = []

grid_solver_HGBC = GridSearchCV(estimator      = model_HGBC,
                                param_grid     = parameters_HGBC,
                                scoring        = "accuracy",
                                refit          = "accuracy",
                                cv             = 5,
                                n_jobs         = -1,
                                verbose        = 2)

model_result_HGBC = grid_solver_HGBC.fit(X_train_scaled, y_train)


y_pred = model_result_HGBC.best_estimator_.predict(X_test_scaled)

params_HGBC = model_result_HGBC.best_estimator_.get_params()

# Metrics:
accuracy = accuracy_score(y_test, y_pred)
precision = precision_score(y_test, y_pred)
recall = recall_score(y_test, y_pred)

resultados_HGBC.append([str(model_HGBC), accuracy, precision, recall,␣
 ↪params_HGBC])
resultados.append([str(model_HGBC), accuracy, precision, recall, params_HGBC])
```

```
df_resultados_HGBC = pd.DataFrame(resultados_HGBC, columns= ["Modelo",␣
 ↪"Accuracy", "Precision", "Recall", "Parameters"])
```

[ ]:
```
##########################################################################################
```

3.1.4 3.1.4- XGB Classifier

[514]:
```
model_XGB = XGBClassifier(objective='binary:logistic',
                          eval_metric='aucpr',
                          tree_method='hist',
                          use_label_encoder=False)

parameters_XGB = {'n_estimators'      : [100,150,200],
                  'learning_rate'     : [i/100 for i in range(1,10)],
                  "booster"           : ["gbtree"],
                  "grow_policy"       : ["depthwise", "lossguide"]}
```

[ ]:
```
resultados_XGB = []

grid_solver_XGB = GridSearchCV(estimator      = model_XGB,
                               param_grid     = parameters_XGB,
                               scoring        = "accuracy",
                               refit          = "accuracy",
                               cv             = 5,
                               n_jobs         = -1,
                               verbose        = 2)

model_result_XGB = grid_solver_XGB.fit(X_train_scaled, y_train)


y_pred = model_result_XGB.best_estimator_.predict(X_test_scaled)

params_XGB = model_result_XGB.best_estimator_.get_params()

# Metrics:
accuracy = accuracy_score(y_test, y_pred)
precision = precision_score(y_test, y_pred)
recall = recall_score(y_test, y_pred)

resultados_XGB.append([str(model_XGB), accuracy, precision, recall, params_XGB])
resultados.append([str(model_XGB), accuracy, precision, recall, params_XGB])

df_resultados_XGB = pd.DataFrame(resultados_XGB, columns= ["Modelo",␣
 ↪"Accuracy", "Precision", "Recall", "Parameters"])
```

[ ]:
```
##########################################################################################
```

3.1.5 3.1.5- Suport Vector Machine

[509]:
```
model_SVC = SVC(probability=True)

parameters_SVC = {'C'            : [1],
                  'kernel'       : ['rbf'],
                  'gamma'        : ['scale'],
                  "degree"       : [3, 4]}
```

[ ]:
```
%%time

resultados_SVC = []

grid_solver_SVC = GridSearchCV(estimator      = model_SVC,
                               param_grid     = parameters_SVC,
                               scoring        = "accuracy",
                               refit          = "accuracy",
                               cv             = 5,
                               n_jobs         = -1,
                               verbose        = 2)

model_result_SVC = grid_solver_SVC.fit(X_train_scaled, y_train)


y_pred = model_result_SVC.best_estimator_.predict(X_test_scaled)

params_SVC = model_result_SVC.best_estimator_.get_params()

# Metrics:
accuracy = accuracy_score(y_test, y_pred)
precision = precision_score(y_test, y_pred)
recall = recall_score(y_test, y_pred)

resultados_SVC.append([str(model_SVC), accuracy, precision, recall, params_SVC])
resultados.append([str(model_SVC), accuracy, precision, recall, params_SVC])

df_resultados_SVC = pd.DataFrame(resultados_SVC, columns= ["Modelo",␣
↪"Accuracy", "Precision", "Recall", "Parameters"])
```

[ ]:
```
###################################################################################
```

4 4- Final results

[531]:
```
df_resultados = pd.DataFrame(resultados, columns= ["Modelo", "Accuracy",␣
↪"Precision", "Recall", "Parameters"])
```

[532]:
```
# df_resultados.to_csv("resultados_finales_cardio.csv", index= False, sep= ",")
```

```
[621]: df_resultados.sort_values(by= "Accuracy", ascending= False)
```

```
[621]:                                               Modelo  Accuracy  Precision  \
20                        GradientBoostingClassifier()  0.746144   0.766361
14                        GradientBoostingClassifier()  0.746144   0.766361
17                        GradientBoostingClassifier()  0.746073   0.766242
16                        GradientBoostingClassifier()  0.746073   0.766242
15                        GradientBoostingClassifier()  0.746073   0.766242
18                        GradientBoostingClassifier()  0.746073   0.766325
19                        GradientBoostingClassifier()  0.746001   0.766206
13                        GradientBoostingClassifier()  0.745069   0.765815
11                        GradientBoostingClassifier()  0.744495   0.765523
12                        GradientBoostingClassifier()  0.744495   0.765523
7                         GradientBoostingClassifier()  0.743993   0.764276
21                        GradientBoostingClassifier()  0.743777   0.761802
10                        GradientBoostingClassifier()  0.743777   0.762369
9                     HistGradientBoostingClassifier()  0.743275   0.759222
23  XGBClassifier(base_score=None, booster=None, c…  0.742988   0.764008
24                    HistGradientBoostingClassifier()  0.742917   0.764715
5                                                SVC()  0.742630   0.773124
22                               SVC(probability=True)  0.742630   0.773124
25                    HistGradientBoostingClassifier()  0.740980   0.764799
6                                 AdaBoostClassifier()  0.740119   0.780972
8   XGBClassifier(base_score=None, booster=None, c…  0.739258   0.759788
0                                 LogisticRegression()  0.736102   0.764867
3                                    NearestCentroid()  0.722186   0.747559
4                             RandomForestClassifier()  0.719963   0.725346
1                                         GaussianNB()  0.710925   0.757544
2                               KNeighborsClassifier()  0.700739   0.702288

      Recall                                        Parameters
20  0.707723  {'ccp_alpha': 0.0, 'criterion': 'friedman_mse'…
14  0.707723  {'ccp_alpha': 0.0, 'criterion': 'friedman_mse'…
17  0.707723  {'ccp_alpha': 0.0, 'criterion': 'friedman_mse'…
16  0.707723  {'ccp_alpha': 0.0, 'criterion': 'friedman_mse'…
15  0.707723  {'ccp_alpha': 0.0, 'criterion': 'friedman_mse'…
18  0.707580  {'ccp_alpha': 0.0, 'criterion': 'friedman_mse'…
19  0.707580  {'ccp_alpha': 0.0, 'criterion': 'friedman_mse'…
13  0.705570  {'ccp_alpha': 0.0, 'criterion': 'friedman_mse'…
11  0.704421  {'ccp_alpha': 0.0, 'criterion': 'friedman_mse'…
12  0.704421  {'ccp_alpha': 0.0, 'criterion': 'friedman_mse'…
7   0.705139                                              None
21  0.708872  {'ccp_alpha': 0.0, 'criterion': 'friedman_mse'…
10  0.707867  {'ccp_alpha': 0.0, 'criterion': 'friedman_mse'…
9   0.712030                                              None
23  0.702699  {'objective': 'binary:logistic', 'base_score':…
24  0.701263  {'categorical_features': None, 'class_weight':…
```

```
5   0.686334                                                None
22  0.686334  {'C': 1, 'break_ties': False, 'cache_size': 20…
25  0.695521  {'categorical_features': None, 'class_weight':…
6   0.666954                                                None
8   0.699254                                                None
0   0.681309                                                None
3   0.670399                                                None
4   0.707436                                                None
1   0.619868                                                None
2   0.696239                                                None
```

4.0.1 4.1- Gradient Boosting Classifier - Best performance:

[620]:
```
GBC = GradientBoostingClassifier()

param_GBC = {"learning_rate"          : [0.09],
             "loss"                   : ['log_loss'],
             "n_estimators"           : [250],
             "subsample"              : [1],
             "min_impurity_decrease"  : [0.05],
             "max_depth"              : [3]}

GS_GBC = GridSearchCV(estimator      = GBC,
                      param_grid     = param_GBC,
                      scoring        = "accuracy",
                      refit          = "accuracy",
                      cv             = 5,
                      n_jobs         = -1,
                      verbose        = 0)

best_results_GBC = GS_GBC.fit(X_train_scaled, y_train)

# filename = 'final_model.sav'
# pickle.dump(model, open(filename, 'wb'))

y_pred = best_results_GBC.best_estimator_.predict(X_test_scaled)

best_parameters = best_results_GBC.best_estimator_.get_params()

# Metricas:
print(f"Precision = {precision_score(y_test, y_pred)}")
print(f"Recall = {recall_score(y_test, y_pred)}")
print(f"Final model Accuracy = {accuracy_score(y_test, y_pred)}")
```

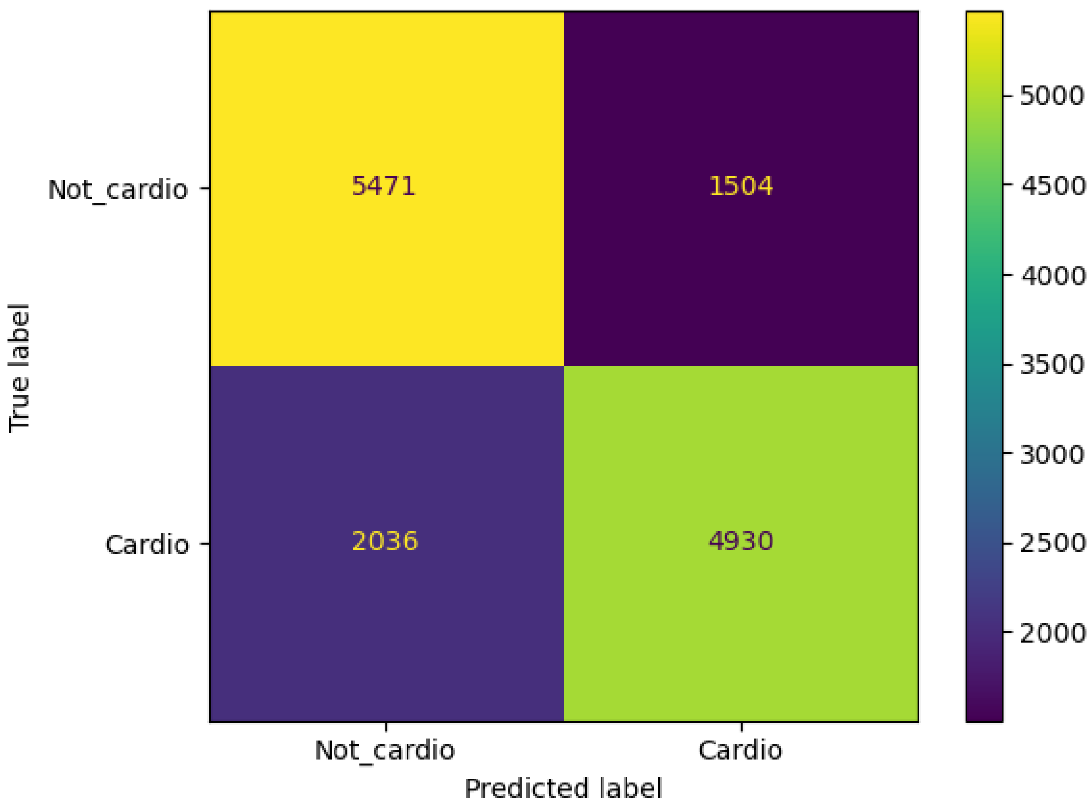
```
Precision = 0.766241840223811
Recall = 0.7077232271030721
Final model Accuracy = 0.7460727350979126
```

```
[619]: dumb_acc = df_processed["cardio"].sum() / len(df_processed)
print(f"Dumb model Accuracy = {dumb_acc}")
```

```
Dumb model Accuracy = 0.49966285525730597
```

```
[ ]: total = Counter(y_test)
print(f"Healthy individuals: {total[0]}\nUnhealthy individuals.: {total[1]}")
```

```
[603]: labels = ["Not_cardio", "Cardio"]
cm = confusion_matrix(y_test, y_pred)
disp = ConfusionMatrixDisplay(confusion_matrix= cm, display_labels= labels)
disp.plot()
plt.show()
```



5 5-Conclusion

*

After experimenting with hyperparameter tuning across various models, we achieved an accuracy of 74.6% with the GradientBoostingClassifier. Considering that the baseline model yields an accuracy of 49.9%, our model has demonstrated a significant improvement in predicting cardiovascular problems. However, further enhancements would be needed to achieve a higher accuracy or, at the very least, a higher recall at the expense of precision.*

[ ]:
```

```